

FIGURE 1

CCGCGGGAACGCTGTCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGCCCGCGCCCAG
 TC**ATG**ACCCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGCTCAGTGCGGGCGGTGTGCCGGG
 CTGAGGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAAACCAT
 GTGCCGAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTG
 ACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAAGCTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGTC
 TTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCATGGAACCGGGGATTTC
 CACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGC
 TAAAGCTGGTGAAGGGCATTTTGCCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATC
 ACCTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAA
 AGAAAT**TAA**TAAATAATAAATTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

FIGURE 2

GCGGAAGTGGCTCCGGCTGGCACCTGAGGAGCGCGTGACCCGAGGGCCAGGGAGCTGCCGGCTGGCCTAGG
 CAGGCAGCCGACCA**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCTGCTCAGCTTCTGGGCATGGTGGGCA
 CGTTGATCACCAACCATCTGCCGCACTGGCGGAGGACAGCGCACGTGGGCACCAACATCCTCAGGCCCGTGTCTCT
 ACCTGAAAGGGCTCTGGATGGAGTGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGC
 TGGCGCTGCCCCAAGACCTCCAGGCTGCCCGCGCCCTCATGGTCATCTCTGCTGCTCTCGGGCATAGCCTGCG
 CCTGCGCCGTCATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACCACCTTTGCCATCCTCG
 GCGGCACCCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGCTCTCTGGACCACCAACGACGTGGTGCAGA
 ACTTCTACAACCCGCTGCTGCCAGCGCATGAAGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCT
 CGTCCCTCTCGCTCATTTGGTGGCACCCCTGCTTTGCCTGTCTGCCAGGACGAGGCACCCCTACAGGCCCTACCAGG
 CCCC GCCAGGGCCACCACGACCACTGCAAAACACCGCACCTGCCACAGGCCACAGCTGCCTACAAAGACAATC
 GGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG**TGA**GTCCCCACAGCCTGCT
 TCTCCCCCTGGGCTGCTGTGGGCTGGGTCCCGGCGGGACTGTCAATGGAGGCAGGGGTTCCAGCACAAAGTTTAC
 TTCTGGGCAATTTTTGTATCCAAGGAAATAATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGG
 AAATAAGAGGAGGAGAAAGCTCTCTATACCAAGACTGAAAAAAAAAATCCTGTCTGTTTTGTATTTATATAT
 ATATTTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTGGGAGTTTGGTCAGTGGGGTTGGTTTGTG
 ATCCAGGAATAAACCTTGCGGATGTGCTGTTTATAAAAAAAAAAAA

FIGURE 3

CAGGACCAGGTTCTTCTACGCTGGAGCAGCGGGAGACAGCCACCATGCACATCCTCGTGGTCCATGCCATGGTG
 ATCTCTGCTGACGCTGGGCGCGCCTCGAGCCGACGACAGCGAGTTCCAGGCGCTGCTGGACATCTGGTTCCGGAG
 GGAAAGCCATGCCACCAGCCTTCTGGTGGACACATCGGAGGAGCGCTGCTGCTTCTGACTGGCTGAAGCTG
 CGCATGATCCGTTCTGAGGTGCTCCGCTGGTGGACGCGCCTCGAGAGCCTGGAGCCGAGCAGCTGCTGTG
 TTGCTCGAGTCGTTTGGCATCCCGTGTCCAGCATGAGCAAACTCCTCCAGTTCTGAGCCAGGCAAGTGGCCAC
 GACCCCGAGACTCGAGCAGAACTCATGGACAAGAATTACATGGCCCAACTGGTGGAGGTCAGCATGAGCGC
 GGGCGCTCCGGAGGCGAGACTTTCCACTCCTTGTCTCACAGCTCCTCGCCGCCCGCGAGACAGCACAGAGCA
 CCCAAACCAAGAGCAGCCAGAGCAGCCATAGGCCAGGCGCGATTCCGGTGGGACCCAGCTCCGGGTGCTG
 GGCCTCGAGGACGACCTGGCTGGCATGTTCTCCAGATTTTCCCGCTCAGCCCCGACCTCGGTGGCAGAGCTCC
 AGTCCCCCGCCGTGGCCCTCGCCCTCGACGAGGCCCTGGGCCAGGAGCTGGCCCGCGCTCGTCCAGGGCAGCCCC
 GAGGTGCGGGCATCAGGTGCTGTCTCGAGGCCCTCGCCACCTGCTCAGCTCCCCACACGGGGTGGCCCTG
 GTGATGTCATGACACCTAGCCACTTCTGGCTGCCCGTGTCTGGCCAGCTCGCCAGTACACGCGTGTCTG
 CCACAGGACACCGGCTTCTCTCGCTCTTCTGAAGGTGCTCTCGAGATGCTCAGCTGGCTGGACAGCCCTGGC
 GTGGAGGCGGGCCCTCGCGGCACAGCTCAGATGCTTGCCAGCCAGGCTCAGCCGGCGCAGGCTCAGTGT
 GTGCGAGGGGGCTTCTGCGCTCGCCGAGGCCCTGGCCCTCGTCAGGACTGGAGTGGTCAGCTCCACCCTC
 CGTGCCCTCATCGCCAGCTGAGGCTGGAGGAGCTGCTGACTGCATTTCTTCTGCCATCGGGATGCTGCC
 TCCCGCTTTCAGCCTGTAAAGCCGTTGTGGTGGTGAAGTCCCTGCTGCTCGAGGAGGAGGCCCTTGCTGGG
 GGGAGCCGGGTGCGGACGCTGGCAGCTGGAGGCCGTGCGGCTGGGGCCCTCGTCAGGCCCTCTAGTGGACTGG
 CTGGAATGCTGACCCCGAGGTGGTCAGCAGCTGCCCGACCTCGAGCTCAGGCTGCTTCTTCCCGGAGGAG
 GGCAAAGGTGAGGCCCGAGTGCCTGTTCCGTCCTACCTCTGACCTCTTACGCACTCAGTCAGGCTGGCCG
 ACATCGACCAAGTGCATCCGATCCTGCTGGGCAAGAGCCGGGAACAGAGTTGACCCCTCTGCTCTCTCGGAC
 TTCTCTGGGCTCATCATCATTTCTCGCATCTGGCAGGGCGGGAGCAGCGCACCCGAGAAGCGGGGGAG
 GAGCTGGTGTGCGGGTCCAGGGCCCGGAGCTCATCAGCTGGTGGAGCTGATCCTGGCCGAGGCGGAGACCGG
 AGCCAGGACGGGGACACAGCGCCCTGCAGCTCATCCAGGCCCGGCTGCCCTGCTGCTCAGCTGCTGCTGTGGG
 GACGATGAGAGTGTCAAGGAAGTGACGGAGCAGCTGTGAGGCTGCATCCAGCATGGGGAGACAGCGCTGTGGGA
 AGGCGCTGCCGAGACCTTCTCTGAGCTCTACCTACAGCGGCCGAGCTGCGGGTGCCCGTGCCTGAGTCTCTA
 CTGCACAGCGAGGGCTGCCAGCAGCAGCTGTGCAAGCTGGACGAGCTCATCCACCGCTTCATCAGCTCCTT
 GCGGACACCGAGCTCCCGGGCGTTGGAGAACCGAGGGCGGATGCCAGCATGGCTGCCGGAAGTGGCGGTG
 GCGCACCCGCTGTGCTGCTCAGGCACCTGCCATGATCGCGCGCTCCTGCACGGCCGACCCACCTCAACTTC
 CAGGAGTTCCGGCAGCAGAACCCTGAGCTGCTTCTTGCACTGCTGGGGCTGCTGGAGCTGCTGCAGCCGAC
 GTGTTCCGACGCGAGCACCAGGGGGCGCTGTGGGACTGCCCTCTGCTCCTCATCCGCTGCTGCTGAATTACAG
 AAGTCTCCCGCATCTGGCTGCCCTTCATCAACAAGTTTGTGAGTTTCATCCATAAGTACATTACCTACAATGCC
 CCAGCAGCCATCTCCTTCTGCAGAAAGCAGCCGACCCGCTCCACGACCTGTCTTTCGACAACAGTGACCTGGTG
 ATGCTGAATCCCTCCTTGCAGGGCTCAGCTTGCCAGCAGGACGACAGGACGACCCAGGCTGGACGAAGAG
 GGCAGGAGGAGGAGCTCAGCCGGCTCCTTGCCCTGGTCAGGCTTCCCTGTTACCCCTCTGACCCGGGCGGAG
 ATGGCCCTACATGAAGCGGCTTTCCCGGGCCAAACGCTGGAGGATCTGCTGGAGGTTCTGAGTGACATAGAC
 GAGATGTCCGGGCGAGGACCCGAGATCCTGAGCTTCTTCTGCACCACTCGACGGCTGATGAGCTCGGCCGAG
 GAGTGTTCGCGCACTCGCCTTACGCTGGCCCTGCGCTCCTGAGAACAGCCAGCATTTGCAGCCGCTTTC
 CTGCCACGTTTCATGTACTGCTGGGCAAGCAGGACTTTGAGGTGGTGCACAGGGCCCTCCGGAACCTGCTCATG
 TAGCTCTCCTGTGCGCAAGAGCAGCGGCTGTGCTGTCTCACCGGGCTTCTGGTGGGATGTACGCGCAGATG
 GACCCCGAGCGGAGATCTCCGAGGCCCTGAGGATCCTGCATATGAGGCGGTGATTGAAGCCTGTGGCACCGGA
 CCCCCCTCAAGCCCGCGCCCTCCCTCCCGGGATCCTCGAGCAAGCCAGGAGGCTGGGGCTTGTCTGG
 TCTGTCCAGGAGGTGAGGGCGCGAGCCCTGAGGCCAGGCAAGCCAGGACGAATACTCCAGGCCCTGGGGTGG
 CTCGGGCGGCGCTGGCATCAGGGCCCTCCAGCAAGCCCTCACTCACTTCTGGGCGACGCCCTGCCGGG
 AGCGCGGATCCCCCGGCATGGCTGGGCTGGTTTTGAATGAACGACCTGACTGTCAA

FIGURE 5

MTLRPSLLPLHLHLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHIHYTGSLVDGRIID
TSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRAIIPSHLAYGKRGFPPSPVADAVVQYDVELIALIRANYWL
KLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVSKKLKEEKRNKSKKK

Signal peptide.

amino acids 1-25

Transmembrane domain.

amino acids 155-174

N-glycosylation site.

amino acids 196-200

N-myristoylation site.

amino acids 95-101

Amidation site.

amino acids 119-123

FKBP-type peptidyl-prolyl cis-trans isomerase signature 1.

amino acids 62-78, 87-124, 128-142

FIGURE 6

MASTAVQLLGFLLSFLGMVGTLLITILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIYQCQIYRSLALPO
DLQAARALMVISCLLSGIACACAVIGMKCTRCAGTTPAKTTFAILGGTLFILAGLLCMVAVSWTTNDVVQNFYNP
LLPSGMKFIEIGQALYLGFISSSLSIGGTLCLSCQDEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSV
TSATHSGYRLNDYV

Signal sequence.

amino acids 1-21

Transmembrane domains.

amino acids 78-98, 116-136, 162-182

N-myristoylation sites.

amino acids 17-22, 20-25, 60-65, 92-97, 101-106, 178-183

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 85-95, 87-97

PMP-22/EMP/MP20/Claudin family.

amino acids 4-181

FIGURE 7

MHILVVHAMVILLTLGPPrADDSFQALLDIWFPEEKPLPTAFIVDTSEEALLLPDWLKLIRMIRSEVLRIVDAAL
 QDLEPQQLLLFVQSFQIPVSSMSKLLQFLDQAVAHDPQTLEQNIMDKNYMAHLEVEVQHERGASGGQTFHSLLTAS
 LPPRRDSTEAFKPKSSPEQPIQGGRIRVGTQLRVLGPEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQ
 ELARVVQGSPEVPGITVRVLQALATILLSSPHGGALVMSMRSHFLACPLLRQLCQYQRCVPQDTGFSSSLFLKVL
 QMLQWLDSPGVEGGPLRAQLRMLASQASAGRRLSDVRGGLRLRLAEALAFRQDLEVVSVSTVRAVIATLRSGEQCSV
 EPDLISKVLQGLIEVRSPHLEELLTAFFSATADAASPPACKPVVVVSSLLQEEEPAGGKPGADGGSLEAVRL
 GPSGGLLDVLEMLDPEVVSSCPDLQLRLFSRRKGKGQAQVPSFRPYLLTLFTHQSSWPTLHQCIRVLLGKSRE
 QRFDPSASLDLFWACIHVPRIWQGRDQRTPKRRREELVLRVQGPELISLVELILAEAEATRSQDGDTAACSLIQAR
 LPLLLSCCGDDESVRKVTEHLSGCIQQWGDVSLGRRCRDLLQLYLRQFELRVVPVEVLLHSEGAASSSVCKLD
 GLIHRFITLLADTSDSRALENRGADASMACRKLAVAHPLLLLRHLPMAALLHGRTHLNFQEFRRQNNHLSCLH
 LGLELLQPHVFRSEHQALWDCLLSFIRLLLNRYKSSRHAAAFINKFVQFIHKYITYNAPAAISFLQKHADPLH
 DLSFDNSDLVMLKSLLAGLSLPSRDDTRDLDEEGEEESSAGSLPLVSVSLFTPLTAAMAPYMKRLSRGQVTE
 DLLEVLSDIDEMSRRRPEILSFFSTNLQRLMSSAECCRNLAFLALRSMQNSPSIAAAFLPTFMYCLGSQDFEV
 VQTALRNLFPEYALLCQHEAAVLLHRAFLVGMYGQMDPSAQISEALRILHMEAVM

Signal peptide.

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449, 665-671,
 698-704

Amidation sites.

amino acids 329-333, 634-638

FIGURE 8

MASLGQILFWSIIISIIIIILAGAIALLIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEFDIKLSDIVIQWLKEG
 VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAF
 SMPEVNVVDYNASSETLRCAPRWFFQPTVVWASQVDQGANFSEVSNTSFEIENSENTMKVVSVLNVNTINNTYSC
 MIENDIAKATGDIKVTSEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYMLLK

Signal peptide.

amino acids 1-28

Transmembrane domain.

amino acids 258-281

N-glycosylation sites.

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220, 220-224

N-myristoylation sites.

amino acids 52-58, 126-132, 188-194

Immunoglobulin domain.

amino acids 49-132